

POLYMER LETTERS

<120> Groups of *Borrelia burgdorferi* and
Borrelia afzelii That Cause Lyme Disease in Humans

<150> US 60/140,042
<151> 1999-06-18

<170> FastSEQ for Windows Version 4.0

<220>
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<220>
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<211> 573
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<220>
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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser 15
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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 30
20 25

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 45
35 40

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile 60
50 55

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 80
65 70 75

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser 95
85 90

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys 110
100 105

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln 125
115 120

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu 140
130 135

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys 160
145 150 155

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu 175
165 170

Sub A1

0056745-061900

3/102

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu 175
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gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat gga tcc 573
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180 185

<210> 6
<211> 190
<212> PRT
<213> borrelia burgdorferi

<400> 6
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Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu 45
35 40
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys 60
50 55
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu 80
65 70 75
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys 95
85 90
Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys 110
100 105
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu 125
115 120
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys 140
130 135
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu 160
145 150 155
Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 175
165 170
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Ser 190
180 185

<210> 7
<211> 557
<212> DNA
<213> Borrelia burgdorferi

<220>
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<222> (1)...(557)

<400> 7
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1 5 10

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 30
20 25

0050715-05100

Sub A1

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
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 35 40 45
 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60
 ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65 70 75 80
 tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85 90 95
 gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
 100 105 110
 tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 115 120 125
 ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
 130 135 140
 aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 145 150 155 160
 aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
 165 170 175
 gct gtt aaa gag ctt aca agt cct att gt 557
 Ala Val Lys Glu Leu Thr Ser Pro Ile
 180 185

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 <212> PRT
 <213> Borrelia burgdorferi

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 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
 35 40 45
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
 50 55 60
 Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu
 65 70 75 80
 Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val
 85 90 95

SubA1

00506716-061000

Sub A1

Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys
 100 105 110
 Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly
 115 120 125
 Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys
 130 135 140
 His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys
 145 150 155 160
 Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala
 165 170 175
 Val Lys Glu Leu Thr Ser Pro Ile
 180

<210> 9
 <211> 579
 <212> DNA
 <213> Borrelia burgdorferi

<220>
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 <222> (1)...(579)

<400> 9
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 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30
 aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144
 Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
 35 40 45
 gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att gct gct 192
 Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala
 50 55 60
 aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat acc gaa 240
 Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu
 65 70 75 80
 aat aat cac aat gga tca ttg tta gcg gga gct tat gca ata tca acc 288
 Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
 85 90 95
 cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta aag gaa 336
 Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu
 100 105 110
 aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat aaa tta 384
 Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu
 115 120 125
 aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat gct gat 432
 Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp
 130 135 140

Sub A1

gca aaa gaa ggc att tta aaa aca aat ggt act aaa act aaa ggt gct	480
Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala	
145 150 155 160	
gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca aaa gca	528
Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala	
165 170 175	
gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct gtt	576
Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val	
180 185 190	
gtg	579
Val	

<210> 10
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 <212> PRT
 <213> Borrelia burgdorferi

<400> 10

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Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val	
35 40 45	
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys	
50 55 60	
Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn	
65 70 75 80	
Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu	
85 90 95	
Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys	
100 105 110	
Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys	
115 120 125	
Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala	
130 135 140	
Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu	
145 150 155 160	
Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala	
165 170 175	
Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val	
180 185 190	

<210> 11
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 <213> Borrelia brgdorferi

<220>
 <221> CDS
 <222> (1)...(582)

006190-061900

SubA1

<400> 11
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aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30

aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144
 Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
 35 40 45

gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt gct aaa 192
 Val Lys Glu Val Glu Ala Leu Ser Ser Ile Asp Glu Leu Ala Lys
 50 55 60

gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat gaa gca 240
 Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala
 65 70 75 80

aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca acc tta 288
 Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu
 85 90 95

ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta aag gaa 336
 Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu
 100 105 110

aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act aaa cta 384
 Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu
 115 120 125

aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat gaa aat 432
 Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn
 130 135 140

gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat aag ggc 480
 Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly
 145 150 155 160

gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta tca aaa 528
 Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys
 165 170 175

gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct 576
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
 180 185 190

gtt gtg
 Val Val 582

<210> 12
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 <212> PRT
 <213> Borrelia burgdorferi

005945-063600

<400> 12

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 35 40 45
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala
 50 55 60
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn
 65 70 75 80
 Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile
 85 90 95
 Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys
 100 105 110
 Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys
 115 120 125
 Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala
 130 135 140
 Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val
 145 150 155 160
 Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala
 165 170 175
 Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val
 180 185 190
 Val

<210> 13

<211> 576

<212> DNA

<213> Borrelia burgdorferi

<220>

<221> CDS

<222> (1)...(576)

<400> 13

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 1 5 10 15
 aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30
 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45
 gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192
 Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
 50 55 60
 aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc aat cag 240
 Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
 65 70 75 80

SubA1

006T220-949560

agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta 288
 Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu
 85 90 95
 ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag 336
 Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys
 100 105 110
 att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa 384
 Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys
 115 120 125
 agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca 432
 Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala
 130 135 140
 caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca 480
 Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
 145 150 155 160
 gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528
 Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
 165 170 175
 caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576
 Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
 180 185 190

<210> 14
 <211> 191
 <212> PRT
 <213> Borrelia burgdorferi

<400> 14
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 35 40 45
 Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
 50 55 60
 Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser
 65 70 75 80
 Lys Asn Thr Ser Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile
 85 90 95
 Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile
 100 105 110
 Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser
 115 120 125
 Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln
 130 135 140
 Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu
 145 150 155 160
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln
 165 170 175

00596746-051900

Sub A1

[illegible]

gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
165 170 175

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576
 Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
 180 185 190

<210> 16
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 <212> PRT
 <213> borrelia burgdorferi

<400> 16
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 20 25 30
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 35 40 45
 Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys
 50 55 60
 Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser
 65 70 75 80
 Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile
 85 90 95
 Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile
 100 105 110
 Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser
 115 120 125
 Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln
 130 135 140
 Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu
 145 150 155 160
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln
 165 170 175
 Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
 180 185 190

<210> 17
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 <213> Borrelia burgdorferi

<220>
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<400> 17
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 1 5 10 15
 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30
 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45

005190-943650

Sub A1

gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa 192
 Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys
 50 55 60
 gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca 240
 Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala
 65 70 75 80
 gat cac aac gga tca tta ata tca gga gca tat tta att tca aac tta 288
 Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu
 85 90 95
 ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca 336
 Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala
 100 105 110
 gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta 384
 Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu
 115 120 125
 aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat 432
 Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn
 130 135 140
 gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc gct 480
 Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala
 145 150 155 160
 gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca 528
 Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala
 165 170 175
 gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc cct 573
 Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro
 180 185 190

<210> 18
 <211> 190
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 <213> Borrelia burgdorferi

<400> 18
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 1 5 10 15
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 20 25 30
 Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val
 35 40 45
 Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala
 50 55 60
 Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp
 65 70 75 80
 His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile
 85 90 95
 Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu
 100 105 110

00596745-051900

Sub A1

Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys
 115 120 125
 Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala
 130 135 140
 Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp
 145 150 155 160
 Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala
 165 170 175
 Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro
 180 185 190

<210> 19
 <211> 553
 <212> DNA
 <213> *Borrelia burgdorferi*

<220>
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 <222> (1)...(553)

<400> 19
 atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg 48
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 aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 20 25 30
 aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct 144
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 35 40 45
 gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act 192
 Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
 50 55 60
 aaa gct att ggt aaa aaa ata gat aac aat gct ggt ttg ggt gct gaa 240
 Lys Ala Ile Gly Lys Lys Ile Asp Asn Asn Ala Gly Leu Gly Ala Glu
 65 70 75 80
 gtg ggt caa aac gga tca ttg cta gca gga gct tat gca atc tca act 288
 Val Gly Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
 85 90 95
 gta ata ata gaa aaa ttg agc aca tta aaa aat gta gaa gaa tta aaa 336
 Val Ile Ile Glu Lys Leu Ser Thr Leu Lys Asn Val Glu Glu Leu Lys
 100 105 110
 gaa aaa att aca aag gct aag gat tgt tct gaa aaa ttc act aaa aaa 384
 Glu Lys Ile Thr Lys Ala Lys Asp Cys Ser Glu Lys Phe Thr Lys Lys
 115 120 125
 tta aaa gat agc cgc gca gag ctt ggt aaa aaa gat gcc agt gat gat 432
 Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp
 130 135 140

[illegible]

gcg gct aaa gag atg cta aac aag t 553
Ala Ala Lys Glu Met Leu Asn Lys
180

[illegible]

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<220>  
<221> CDS  
<222> (1) ... (582)
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<400> 21
atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg 48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
1 5 10 15

[illegible]

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<210> 22
<211> 193
<212> PRT
<213> Borrelia burgdorferi
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~~<400> 22
Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn
1 5 10 15
Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr
20 25 30~~

SECRET

<220>
<223> OspC Chimera

<400> 23																
atg	gct	tgt	aat	aat	tca	ggg	aaa	gat	ggg	aat	aca	tct	gca	aat	tct	48
Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	
1				5					10					15		
gct	gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	96
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	
			20					25					30			
att	acg	gat	tct	aat	gcg	gtt	tta	ctt	gct	gtg	aaa	gag	gtt	gaa	gcg	144
Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	
		35				40						45				
ttg	ctg	tca	tct	ata	gat	gaa	att	gct	gct	aaa	gct	att	ggt	aaa	aaa	192
Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile	Ala	Ala	Lys	Ala	Ile	Gly	Lys	Lys	
	50					55				60						
ata	cac	caa	aat	aat	ggt	ttg	gat	acc	gaa	tat	aat	cac	aat	gga	tca	240
Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	
65					70					75					80	

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
 180 185 190

atg gta aat aat tca ggg aaa gat ggg aat aca tct gca aat tct gct 624
 Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 195 200 205

gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 210 215 220

aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg 720
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
 225 230 235 240

ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata aaa 768
 Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
 245 250 255

aac gat gtt agt tta gat aat gag gca gat cac aac gga tca tta ata 816
 Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile
 260 265 270

tca gga gca tat tta att tca aac tta ata aca aaa aaa ata agt gca 864
 Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala
 275 280 285

ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct aag aaa 912
 Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys
 290 295 300

tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca gat ctt 960
 Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu
 305 310 315 320

00596745-051900

Sub A1

Sub A1

ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att tta aaa 1008
 Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
 325 330 335

aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag tta ttt 1056
 Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe
 340 345 350

gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt act aat 1104
 Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn
 355 360 365

tca gtt aaa gag ctt aca agc taa 1128
 Ser Val Lys Glu Leu Thr Ser *
 370 375

<210> 24
 <211> 374
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 24
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 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 20 25 30
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 35 40 45
 Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60
 His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu
 65 70 75 80
 Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
 85 90 95
 Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
 115 120 125
 Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
 130 135 140
 Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
 145 150 155 160
 Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
 165 170 175
 Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met
 180 185 190
 Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp
 195 200 205
 Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr
 210 215 220
 Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu
 225 230 235 240
 Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn
 245 250 255

006129 9436560

Sub A1

Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser 270
 Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile 285
 Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys 300
 Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly 320
 Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr 335
 Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu 350
 Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser 365
 Val Lys Glu Leu Thr Ser 370

<210> 25
 <211> 1124
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OSpC Chimera

<221> CDS
 <222> (1)...(1124)

<400> 25
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser 15
 1 5 10
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys 30
 20 25
 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala 45
 35 40
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys 60
 50 55
 ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser 80
 65 70 75
 ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 95
 85 90
 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 110
 100 105

20/102

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
 180 185 190
 atg gta aat aat tca gga aaa gat ggg aat aca tct gca aat tct gct 624
 Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 195 200 205
 gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 210 215 220
 aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg 720
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu
 225 230 235 240
 ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa aaa ata 768
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
 245 250 255
 caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg 816
 Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu
 260 265 270
 tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa tta gat 864
 Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp
 275 280 285
 gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat gct aag 912
 Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys
 290 295 300
 aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat gcg caa 960
 Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln
 305 310 315 320
 ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct att tta 1008
 Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 325 330 335
 ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa aag cta 1056
 Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
 340 345 350

0059716-061600

Sub A1

Sub A1

ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg ctt gct 1104
 Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala
 355 360 365

aat tca gtt aaa gag ctt ac
 Asn Ser Val Lys Glu Leu
 370

1124

<210> 26
 <211> 373
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 26
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 1 5 10 15
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 20 25 30
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 35 40 45
 Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60
 His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu
 65 70 75 80
 Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
 85 90 95
 Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
 115 120 125
 Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
 130 135 140
 Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
 145 150 155 160
 Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
 165 170 175
 Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala Met
 180 185 190
 Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp
 195 200 205
 Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr
 210 215 220
 Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu
 225 230 235 240
 Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln
 245 250 255
 Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu
 260 265 270
 Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly
 275 280 285
 Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys
 290 295 300
 Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu
 305 310 315 320

006750 061000

Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile
 325 330 335
 Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 340 345 350
 Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn
 355 360 365
 Ser Val Lys Glu Leu
 370

<210> 27
 <211> 1137
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1137)

<400> 27
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
 20 25 30
 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65 70 75 80
 ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140

0059746-061900

Sub A1

23/102

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 160
 145 150 155
 ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 175
 165 170
 aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 576
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys 190
 180 185
 aaa cct tcc atg gta aat aat tca ggg aaa gat ggg aat aca tct gca 624
 Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala 205
 195 200
 aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt 672
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser 220
 210 215
 aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt 720
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val 240
 225 230 235
 gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa 768
 Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys 255
 245 250
 aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga 816
 Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly 270
 260 265
 tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa 864
 Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys 285
 275 280
 ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag 912
 Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys 300
 290 295
 gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac 960
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His 320
 305 310 315
 aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc 1008
 Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala 335
 325 330
 att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa 1056
 Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu 350
 340 345
 aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg 1104
 Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met 365
 355 360
 ctt act aat tca gtt aaa gag ctt aca agc taa 1137
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser * 375
 370 375

Sub A1

00595745-051900

SubA1
 <210> 28
 <211> 378
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 28
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 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
 20 25 30
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65 70 75 80
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
 180 185 190
 Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
 195 200 205
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 210 215 220
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
 225 230 235 240
 Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
 245 250 255
 Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
 260 265 270
 Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
 275 280 285
 Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
 290 295 300
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
 305 310 315 320
 Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
 325 330 335
 Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
 340 345 350
 Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
 355 360 365
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 370 375

00691600

Sub A1
 <210> 29
 <211> 1133
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1133)

<400> 29
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 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
 20 25 30
 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65 70 75 80
 ttg tta gcg gga gct tat gaa ata tca acc cta ata aaa caa aaa tta 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175

Sub A1

THE UNIVERSITY OF CHICAGO

```
<210> 30
<211> 377
<212> PRT
<213> Artificial Sequence
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~~<220>~~ ~~OspC Chimera~~

~~<400> 30~~
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
10 15

Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala

Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
50 55 60 75 80

Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys

Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu

Lys Ala Asn Gly Thr 150 155 160
145 Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
Phe Glu Ser Val Glu Val Leu Ser Lys Ala 175

Asn Ser Val Lys Gln Lys 185 190
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala

Asn Ser Ala Asp Glu Ser Val Leu Ile
210 220

Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
230 240

Glu Thr Leu Leu Ala Ser His Asp His 250 255
 245
 Leu Leu Ile Gln Gln Asp Gly Gly Leu Ala Val Glu Ala Gly His Asn

Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys 285
275
Glu Leu Lys Asp Ser Glu Lys Leu Lys Glu Lys Ile Glu

Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Ser Thr 320
305 310 315
Glu Asp Val Thr Asp Glu Asn Ala Lys Lys

Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
340 345
Asp Val Glu Asp Leu Ala Lys Ala Ala Lys Glu

Met Leu Ala Asn Ser Val Lys Glu Leu
370 375

<211> 1112

<213> Art

TABLE 1. *Continued*

<223> OspC Chimera

$\langle 222 \rangle$ (1) ... (1112)

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~~Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser~~
~~1 5 10 15~~

gct gat gag tdt gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
180 185 190

tca aga aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt 624
Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val
195 200 205

SECRET

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac 672
 Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
 210 215 220
 gca gtt ggt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata 720
 Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile
 225 230 235 240
 gat gaa ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt 768
 Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly
 245 250 255
 tta gag gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat 816
 Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr
 260 265 270
 gca ata tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa 864
 Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu
 275 280 285
 gaa tta aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt 912
 Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe
 290 295 300
 act aat aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt 960
 Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu
 305 310 315 320
 act gat gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa 1008
 Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys
 325 330 335
 gat aag ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac 1056
 Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
 340 345 350
 tta tca aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt 1104
 Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu
 355 360 365
 aca agt cc 1112
 Thr Ser
 370

<210> 32
 <211> 369
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

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 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 20 25 30

00596745-051500

SubA1

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Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 35 40 45
 Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
 50 55 60
 Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu
 65 70 75 80
 Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys
 85 90 95
 Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
 115 120 125
 Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
 130 135 140
 Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
 145 150 155 160
 Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
 180 185 190
 Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys
 195 200 205
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 210 215 220
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp
 225 230 235 240
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu
 245 250 255
 Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala
 260 265 270
 Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu
 275 280 285
 Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr
 290 295 300
 Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr
 305 310 315 320
 Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp
 325 330 335
 Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu
 340 345 350
 Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr
 355 360 365
 Ser

<210> 33
 <211> 1113
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1113)

<400> 33

006746-051000

Sub A1

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 1 5 10 15
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60
 aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80
 tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95
 aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
 100 105 110
 aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115 120 125
 ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 130 135 140
 aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
 145 150 155 160
 ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175
 gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180 185 190
 tca ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt 624
 Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val
 195 200 205
 aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac 672
 Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
 210 215 220
 gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata 720
 Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile
 225 230 235 240

Sub A1

005746-051000

Sub A1

gat gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt	768
Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser	
245 250 255	
tta gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat	816
Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr	
260 265 270	
tta att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca	864
Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser	
275 280 285	
gga gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa	912
Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu	
290 295 300	
ttt act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc	960
Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly	
305 310 315 320	
gtt act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat	1008
Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp	
325 330 335	
aaa act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa	1056
Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys	
340 345 350	
aac ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag	1104
Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu	
355 360 365	
ctt aca agc	1113
Leu Thr Ser	
370	

<210> 34
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

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Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu	
35 40 45	
Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys	
50 55 60	
Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Leu	
65 70 75 80	
Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser Lys	
85 90 95	

006T90-54296560

Sub-A1

Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys Lys
100 105 110
Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln Leu
115 120 125
Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Lys
130 135 140
Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys Leu
145 150 155 160
Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
180 185 190
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
195 200 205
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
210 215 220
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
225 230 235 240
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
245 250 255
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
260 265 270
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
275 280 285
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
290 295 300
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
305 310 315 320
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
325 330 335
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
340 345 350
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
355 360 365
Thr Ser
370

<210> 35
<211> 1112
<212> DNA
<213> Artificial Sequence

<220>
<223> OSpC Chimera

<221> CDS
<222> (1)...(1112)

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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
 100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
 145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180 185 190

tca gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt 624
 Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val
 195 200 205

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac 672
 Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
 210 215 220

gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata 720
 Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile
 225 230 235 240

gat gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt 768
 Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly
 245 250 255

ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct 816
 Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala
 260 265 270

005745-051000

Sub-A1

Sub A1

tat	aca	ata	tca	aaa	cta	ata	aca	caa	aaa	tta	gat	gga	ttg	aaa	aat	864
Tyr	Thr	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	
		275					280					285				
tca	gaa	aaa	tta	aag	gaa	aaa	att	gaa	aat	gct	aag	aaa	tgt	tct	gaa	912
Ser	Glu	Lys	Leu	Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser	Glu	
		290				295					300					
gat	ttt	act	aaa	aaa	cta	gaa	gga	gaa	cat	gcg	caa	ctt	gga	att	gaa	960
Asp	Phe	Thr	Lys	Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile	Glu	
					310					315					320	
aat	gtt	act	gat	gag	aat	gca	aaa	aaa	gct	att	tta	ata	aca	gat	gca	1008
Asn	Val	Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp	Ala	
				325					330					335		
gct	aaa	gat	aag	ggc	gct	gca	gag	ctt	gaa	aag	cta	ttt	aaa	gca	gta	1056
Ala	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	
			340					345					350			
gaa	aac	ttg	gca	aaa	gca	gct	aaa	gag	atg	ctt	gct	aat	tca	gtt	aaa	1104
Glu	Asn	Leu	Ala	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	
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gag	ctt	ac														1112
Glu	Leu															
		370														

<210> 36
 <211> 369
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 36

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Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	
			20					25					30			
Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	
			35				40					45				
Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	
	50					55					60					
Asn	Asp	Gly	Ser	Leu	Asp	Asn	Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu	Leu	
	65				70				75					80		
Ala	Gly	Ala	Tyr	Thr	Ile	Ser	Thr	Leu	Ile	Thr	Gln	Lys	Leu	Ser	Lys	
			85					90					95			
Leu	Asn	Gly	Ser	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Ala	Ala	Ala	Lys	Lys	
			100					105				110				
Cys	Ser	Glu	Phe	Ser	Thr	Lys	Leu	Lys	Asp	Asn	His	Ala	Gln	Leu		
		115				120					125					
Gly	Ile	Gln	Gly	Val	Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	
	130					135					140					
Ala	Asn	Ala	Ala	Gly	Lys	Asp	Lys	Gly	Val	Glu	Glu	Leu	Glu	Lys	Leu	
	145				150					155					160	

006746-061900

Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn Ser
 180 185 190
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 195 200 205
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 210 215 220
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp
 225 230 235 240
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly
 245 250 255
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr
 260 265 270
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser
 275 280 285
 Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
 290 295 300
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
 305 310 315 320
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
 325 330 335
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
 340 345 350
 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
 355 360 365
 Leu

<210> 37
 <211> 1106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1106)

<400> 37
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 1 5 10 15
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45
 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60

0059546.06.90

Sub A1

37/102

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu 80
 65 70 75

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn 95
 85 90

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln 110
 100 105

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu 125
 115 120

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys 140
 130 135

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe 160
 145 150 155

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn 175
 165 170

gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca aga 576
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg 190
 180 185

aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg 624
 Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly 205
 195 200

cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt 672
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val 220
 210 215

gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa 720
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu 240
 225 230 235

ctt gct acc aaa gct att ggt aag aaa ata gcc aat aat ggt tta gag 768
 Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu 255
 245 250

gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata 816
 Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile 270
 260 265

tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta 864
 Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu 285
 275 280

aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat 912
 Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn 300
 290 295

00596745-051000

Sub A1

aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat 960
 Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp
 305 310 315 320
 gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag 1008
 Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys
 325 330 335
 ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca 1056
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser
 340 345 350
 aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt 1104
 Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
 355 360 365
 cc 1106

<210> 38
 <211> 368
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 38
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65 70 75 80
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85 90 95
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
 100 105 110
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 115 120 125
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
 130 135 140
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 145 150 155 160
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
 165 170 175
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg
 180 185 190
 Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly
 195 200 205
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
 210 215 220
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu
 225 230 235 240

0055716-0600

Sub-A1

<220>
<223> OspC Chimera

<400> 39																	
atg	gct	tgt	aat	aat	tca	gga	aaa	gat	ggg	aat	gca	tct	gca	aat	tct	48	
Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Ala	Ser	Ala	Asn	Ser		
1				5					10					15			
gct	gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	96	
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys		
			20					25					30				
att	aca	gaa	tct	aac	gca	gtt	gtt	ctg	gcc	gtg	aaa	gaa	gtt	gag	acc	144	
Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr		
		35					40					45					
tta	ctt	gca	tct	ata	gat	gaa	ctt	gct	acc	aaa	gct	att	ggt	aaa	aaa	192	
Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys		
	50					55					60						
ata	ggc	aat	aat	ggt	tta	gag	gcc	aat	cag	agt	aaa	aac	aca	tca	ttg	240	
Ile	Gly	Asn	Asn	Gly	Leu	Glu	Ala	Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu		
65				70						75					80		
tta	tca	gga	gct	tat	gca	ata	tct	gac	cta	ata	gca	gaa	aaa	tta	aat	288	
Leu	Ser	Gly	Ala	Tyr	Ala	Ile	Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn		
				85					90					95			
gta	ttg	aaa	aat	gaa	gaa	tta	aag	gaa	aag	att	gat	aca	gct	aag	caa	336	
Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln		
			100					105					110				

Sub A1

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt	384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu	
115 120 125	
ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt	480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat	528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
165 170 175	
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca ggg	576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly	
180 185 190	
aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg	624
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly	
195 200 205	
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt	672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val	
210 215 220	
gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag	720
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu	
225 230 235 240	
ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat	768
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp	
245 250 255	
aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta att	816
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile	
260 265 270	
tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa	864
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu	
275 280 285	
ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act	912
Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr	
290 295 300	
gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act	960
Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr	
305 310 315 320	
gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act	1008
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr	
325 330 335	
aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg	1056
Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu	
340 345 350	

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Sub A1
 tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca 1104
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
 355 360 365

1107

agc
 Ser

<210> 40
 <211> 368
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 40
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser Ala 15
 1 5 10
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile 30
 20 25
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu 45
 35 40
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile 60
 50 55 60
 Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu 80
 65 70 75
 Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val 95
 85 90
 Leu Lys Asn Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys 110
 100 105
 Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly 125
 115 120
 Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys 140
 130 135
 His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys 160
 145 150 155
 Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala 175
 165 170
 Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly Lys 190
 180 185
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 205
 195 200
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val 220
 210 215
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu 240
 225 230 235
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn 255
 245 250
 Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser 270
 260 265
 Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu 285
 275 280
 Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala 300
 290 295
 Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 320
 305 310 315

05506746-051900

SubAI

Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys
				325					330					335	
Gly	Ala	Asp	Glu	Leu	Glu	Lys	Leu	Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser
			340					345					350		
Lys	Ala	Ala	Lys	Glu	Met	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser
		355					360						365		

<210> 41
 <211> 1106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1106)

<400> 41

atg	gct	tgt	aat	aat	tca	gga	aaa	gat	ggg	aat	gca	tct	gca	aat	tct	48
Met	Ala	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Ala	Ser	Ala	Asn	Ser	
1				5					10					15		
gct	gat	gag	tct	gtt	aaa	ggg	ctt	aat	ctt	aca	gaa	ata	agt	aaa	aaa	96
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	
			20					25					30			
att	aca	gaa	tct	aac	gca	gtt	gtt	ctg	gcc	gtg	aaa	gaa	gtt	gag	acc	144
Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	
			35				40					45				
tta	ctt	gca	tct	ata	gat	gaa	ctt	gct	acc	aaa	gct	att	ggt	aaa	aaa	192
Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	
		50				55			60							
ata	ggc	aat	aat	ggt	tta	gag	gcc	aat	cag	agt	aaa	aac	aca	tca	ttg	240
Ile	Gly	Asn	Asn	Gly	Leu	Glu	Ala	Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu	
65					70				75						80	
tta	tca	gga	gct	tat	gca	ata	tct	gac	cta	ata	gca	gaa	aaa	tta	aat	288
Leu	Ser	Gly	Ala	Tyr	Ala	Ile	Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn	
				85				90						95		
gta	ttg	aaa	aat	gaa	gaa	tta	aag	gaa	aag	att	gat	aca	gct	aag	caa	336
Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln	
			100					105					110			
tgt	tct	aca	gaa	ttt	act	aat	aaa	cta	aaa	agt	gaa	cat	gca	gtg	ctt	384
Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu	
			115				120					125				
ggt	ctg	gac	aat	ctt	act	gat	gat	aat	gca	caa	aga	gct	att	tta	aaa	432
Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys	
						135					140					

05595746-051000

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 145 150 155 160
 aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
 165 170 175
 gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca gga 576
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly
 180 185 190
 aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg 624
 Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
 195 200 205
 cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt 672
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
 210 215 220
 gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa 720
 Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu
 225 230 235 240
 ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta 768
 Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu
 245 250 255
 gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca 816
 Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr
 260 265 270
 ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa 864
 Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu
 275 280 285
 aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt 912
 Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe
 290 295 300
 act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt 960
 Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val
 305 310 315 320
 act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa 1008
 Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys
 325 330 335
 gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac 1056
 Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
 340 345 350
 ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt 1104
 Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 355 360 365
 ac 1106

<210> 42

00595745-051900

Sub A1

Sub A1
 <211> 367
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 42
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser Ala
 1 5 10 15
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 20 25 30
 Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
 35 40 45
 Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
 50 55 60
 Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu
 65 70 75 80
 Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val
 85 90 95
 Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys
 100 105 110
 Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly
 115 120 125
 Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys
 130 135 140
 His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys
 145 150 155 160
 Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala
 165 170 175
 Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly Lys
 180 185 190
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 195 200 205
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 210 215 220
 Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 225 230 235 240
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala
 245 250 255
 Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile
 260 265 270
 Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys
 275 280 285
 Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr
 290 295 300
 Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr
 305 310 315 320
 Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp
 325 330 335
 Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu
 340 345 350
 Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 355 360 365

<210> 43
 <211> 633
 <212> DNA

<213> Borrelia burgdorferi

<220>

<221> CDS

<222> (1)... (633)

<400> 43

atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48
 Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
 1 5 10 15

ata tct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 96
 Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 20 25 30

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 144
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
 35 40 45

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 192
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 50 55 60

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 240
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 65 70 75 80

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 288
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 85 90 95

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 336
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 100 105 110

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 384
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 115 120 125

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 432
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 130 135 140

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 480
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 145 150 155 160

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 528
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 165 170 175

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 576
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 180 185 190

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt coa aaa 624
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
 195 200 205

Sub A1

00596746-051900

aaa cct taa
Lys Pro *
210

<210> 44
<211> 209
<212> PRT
<213> Borrelia burgdorferi

<400> 44
Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
1 5 10 15
Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
20 25 30
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile
35 40 45
Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
50 55 60
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
65 70 75 80
His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser Leu
85 90 95
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
100 105 110
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
115 120 125
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
130 135 140
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
145 150 155 160
Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
165 170 175
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
180 185 190
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys
195 200 205
Pro

<210> 45
<211> 580
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(580)

<400> 45
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30

006150-9426560

Sub-A1

47/102

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65 70 75 80
 ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca tcc 576
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser
 180 185 190
 atg g 580
 Met

<210> 46
 <211> 192
 <212> PRT
 <213> *Borrelia burgdorferi*

<400> 46
 Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 1 5 10 15
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys Ile
 20 25 30
 Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu
 35 40 45
 Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60

00596745-061900

Sub A1

His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser Leu
 65 70 75 80
 Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp
 85 90 95
 Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys
 100 105 110
 Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu
 115 120 125
 Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys
 130 135 140
 Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe
 145 150 155 160
 Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn
 165 170 175
 Ser Val Lys Glu Leu Thr Ser Pro Val Ala Glu Ser Pro Ser Met
 180 185 190

<210> 47
 <211> 639
 <212> DNA
 <213> Borrelia garinii

<220>
 <221> CDS
 <222> (1)...(639)

<400> 47
 atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48
 Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
 1 5 10 15
 ata tct tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat 96
 Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn
 20 25 30
 cct gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa 144
 Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 35 40 45
 aaa att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag 192
 Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu
 50 55 60
 act ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa 240
 Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln
 65 70 75 80
 aaa ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga 288
 Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly
 85 90 95
 tcg ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa 336
 Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys
 100 105 110
 ttg agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag 384
 Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys
 115 120 125

005745-051900

Sub A1

gct aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat 432
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His
 130 135 140
 gca gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct 480
 Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala
 145 150 155 160
 att tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa 528
 Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys
 165 170 175
 gat tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca 576
 Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala
 180 185 190
 cta act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt 624
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser
 195 200 205
 cca aaa aaa cct taa 639
 Pro Lys Lys Pro *
 210

<210> 48
 <211> 211
 <212> PRT
 <213> Borrelia garinii

<400> 48
 Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
 1 5 10 15
 Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
 20 25 30
 Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 35 40 45
 Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
 50 55 60
 Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
 65 70 75 80
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
 85 90 95
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
 100 105 110
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
 115 120 125
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
 130 135 140
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
 145 150 155 160
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
 165 170 175
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
 180 185 190
 Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
 195 200 205

006190-34256500

Sub A1

<220>
<221> CDS
<222> (1) ... (624)

atg aaa aag aat ~~aca~~ tta agt gcg ata tta atg act tta ttt tta ttt 48
Met Lys Lys Asn ~~Thr~~ Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
1 5 10 15

ata tct tgt aat aat tca ggt ggg gat tct gca tct act aat cct gat 96
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp
20 25 30

gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa att aca 144
Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr
35 40 45

gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt 192
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu
50 55 60

tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat 240
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn
65 70 75 80

gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg ata gca 288
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala
85 90 95

gga gct tat gaa ata tca aaa cta ata ~~aca~~ caa aaa tta agt gta ttg 336
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu
100 105 110

aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat tgt tcc 384
Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser
115 120 125

caa aaa ttt act act aag cta aaa gat agt cat ~~aca~~ gag ctt ggt ata 432
Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His ~~Ala~~ Glu Leu Gly Ile
130 135 140

caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa aca cat 480
Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His
145 150 155 160

gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca 528
Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser
165 170 175

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cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat tca gtt 576
 Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val
 180 185 190

aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 624
 Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
 195 200 205

<210> 50
 <211> 206
 <212> PRT
 <213> Borrelia afzelii

<400> 50
 Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe Ile
 1 5 10 15
 Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu
 20 25 30
 Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp
 35 40 45
 Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser
 50 55 60
 Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp
 65 70 75 80
 Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly
 85 90 95
 Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn
 100 105 110
 Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln
 115 120 125
 Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln
 130 135 140
 Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly
 145 150 155 160
 Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu
 165 170 175
 Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys
 180 185 190
 Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 195 200 205

<210> 51
 <211> 1680
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1680)

<400> 51
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15

00596746-051900

SubA1

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa																	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys																	
202530																	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg																	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala																	
354045																	
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa																	192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys																	
505560																	
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca																	240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser																	
65707580																	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta																	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu																	
859095																	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag																	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys																	
100105110																	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat																	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp																	
115120125																	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta																	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu																	
130135140																	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta																	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu																	
145150155160																	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct																	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala																	
165170175																	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc																	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala																	
180185190																	
atg ggt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct																	624
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro																	
195200205																	
gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa																	672
Ala Asp Glu Ser Ala Lys Gly Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys																	
210215220																	
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act																	720
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr																	
225230235240																	
ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa																	768
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys																	
245250255																	

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 816
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
 260 265 270

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg 864
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
 275 280 285

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct 912
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
 290 295 300

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca 960
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
 305 310 315 320

gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att 1008
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
 325 330 335

tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat 1056
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
 340 345 350

tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta 1104
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
 355 360 365

act aat tca gtt aaa gaa ctt ggt cac cgt aat aat tca ggt ggg gat 1152
 Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp
 370 375 380

tct gca tct act aat cct gat gag tct gca aaa gga cct aat ctt acc 1200
 Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr
 385 390 395 400

gta ata agc aaa aaa att aca gat tct aat gca ttt tta ctg gct gtg 1248
 Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val
 405 410 415

aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt tct aaa gct 1296
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala
 420 425 430

att ggt aaa aaa ata aaa aat gat ggt act tta gat aac gaa gca aat 1344
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn
 435 440 445

cga aac gaa tca ttg ata gca gga gct tat gaa ata tca aaa cta ata 1392
 Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile
 450 455 460

aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag aaa aaa att 1440
 Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile
 465 470 475 480

006746-061900

Sub A1

SubA1

aaa gag gct aag gat tgt tcc caa aaa ttt act act aag cta aaa gat	1488
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp	
485 490 495	
agt cat gca gag ctt ggt ata caa agc gtt cag gat gat aat gca aaa	1536
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys	
500 505 510	
aaa gct att tta aaa aca cat gga act aaa gac aag ggt gct aaa gaa	1584
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu	
515 520 525	
ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa	1632
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln	
530 535 540	
gca gca tta act aat tca gtt aaa gag ctt aca aat cct gtt gtg gca	1680
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala	
545 550 555 560	

<210> 52
 <211> 560
 <212> PRT
 <213> ospC Chimera

<400> 52

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
50 55 60	
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro	
195 200 205	
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
210 215 220	
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
225 230 235 240	

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Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
 245 250 255
 Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
 260 265 270
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
 275 280 285
 Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
 290 295 300
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
 305 310 315 320
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
 325 330 335
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
 340 345 350
 Leu Phe Glu Ser Val Glu Gly Leu Lys Ala Ala Gln Val Ala Leu
 355 360 365
 Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp
 370 375 380
 Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr
 385 390 395 400
 Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val
 405 410 415
 Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala
 420 425 430
 Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn
 435 440 445
 Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile
 450 455 460
 Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile
 465 470 475 480
 Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp
 485 490 495
 Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys
 500 505 510
 Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu
 515 520 525
 Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln
 530 535 540
 Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala
 545 550 555 560

<210> 53
 <211> 1137
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1137)

<400> 53
 atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
 100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
 145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180 185 190

tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga 624
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
 195 200 205

cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt 672
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 210 215 220

tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa 720
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
 225 230 235 240

ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat 768
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
 245 250 255

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Sub A1

57/102

aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata 816
 Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
 260 265 270
 tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta 864
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
 275 280 285
 aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act 912
 Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
 290 295 300
 aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat 960
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
 305 310 315 320
 gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag 1008
 Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
 325 330 335
 ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca 1056
 Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
 340 345 350
 aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat 1104
 Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
 355 360 365
 cct gtt gtg gca gaa agt cca aaa aaa cct taa 1137
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
 370 375

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 <211> 378
 <212> PRT
 <213> ospC Chimera

<400> 54
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 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60
 Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115 120 125
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 130 135 140
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
 145 150 155 160

005190-061500

Sub A1

Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180 185 190
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
 195 200 205
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 210 215 220
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
 225 230 235 240
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
 245 250 255
 Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
 260 265 270
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
 275 280 285
 Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
 290 295 300
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
 305 310 315 320
 Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
 325 330 335
 Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
 340 345 350
 Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
 355 360 365
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 370 375

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 <211> 1158
 <212> DNA
 <213> ospC Chimera

<220>
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 <222> (1)...(1158)

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 1 5 10 15
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 att acg gat tct aat gcg gtt tta ctt gct gtt aaa gag gtt gaa gcg 144
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80

[illegible]

ttg Leu	tta Leu	gcg Ala	gga Gly	gct Ala 85	tat Tyr	gca Ala	ata Ile	tca Ser	acc Thr 90	cta Leu	ata Ile	aaa Lys	caa Gln	aaa Lys 95	tta Leu	288
gat Asp	gga Gly	ttg Leu	aaa Lys 100	aat Asn	gaa Glu	gga Gly	tta Leu	aag Lys 105	gaa Glu	aaa Lys	att Ile	gat Asp	gcg Ala 110	gct Ala	aag Lys	336
aaa Lys	tgt Cys	tct Ser 115	gaa Glu	aca Thr	ttt Phe	act Thr	aat Asn 120	aaa Lys	tta Leu	aaa Lys	gaa Glu	aaa Lys 125	cac His	aca Thr	gat Asp	384
ctt Leu	ggt Gly 130	aaa Lys	gaa Glu	ggt Gly	gtt Val	act Thr 135	gat Asp	gct Ala	gat Asp	gca Ala	aaa Lys 140	gaa Glu	gcc Ala	att Ile	tta Leu	432
aaa Lys 145	aca Thr	aat Asn	ggt Gly	act Thr	aaa Lys 150	act Thr	aaa Lys	ggt Gly	gct Ala	gaa Glu 155	gaa Glu	ctt Leu	gga Gly	aaa Lys	tta Leu 160	480
ttt Phe	gaa Glu	tca Ser	gta Val	gag Glu 165	gtc Val	ttg Leu	tca Ser	aaa Lys	gca Ala 170	gct Ala	aaa Lys	gag Glu	atg Met	ctt Leu 175	gct Ala	528
aat Asn	tca Ser	gtt Val 180	aaa Lys	gag Glu	ctt Leu	aca Thr	agc Ser	cct Pro 185	gtt Val	gtg Val	gca Ala	gaa Glu	agt Ser 190	cca Pro	aaa Lys	576
aaa Lys	cct Pro	ttc Phe 195	cat His	ggt Gly	aat Asn	aat Asn	tca Ser 200	ggt Gly	ggg Gly	gat Asp	tct Ser	gca Ala 205	tct Ser	act Thr	aat Asn	624
cct Pro	gat Asp 210	gag Glu	tct Ser	gca Ala	aaa Lys	gga Gly 215	cct Pro	aat Asn	ctt Leu	acc Thr	gta Val 220	ata Ile	agc Ser	aaa Lys	aaa Lys	672
att Ile 225	aca Thr	gat Asp	tct Ser	aat Asn	gca Ala 230	ttt Phe	tta Leu	ctg Leu	gct Ala	gtg Val 235	aaa Lys	gaa Glu	gtt Val	gag Glu	gct Ala 240	720
ttg Leu	ctt Leu	tca Ser	tct Ser	ata Ile 245	gat Asp	gaa Glu	ctt Leu	tct Ser	aaa Lys 250	gct Ala	att Ile	ggt Gly	aaa Lys	aaa Lys 255	ata Ile	768
aaa Lys	aat Asn	gat Asp 260	ggt Gly	act Thr	tta Leu	gat Asp	aac Asn	gaa Glu 265	gca Ala	aat Asn	cga Arg	aac Asn	gaa Glu 270	tca Ser	ttg Leu	816
ata Ile	gca Ala 275	gga Gly	gct Ala	tat Tyr	gaa Glu	ata Ile	tca Ser 280	aaa Lys	cta Leu	ata Ile	aca Thr	caa Gln 285	aaa Lys	tta Leu	agt Ser	864
gta Val 290	ttg Leu	aat Asn	tca Ser	gaa Glu	gaa Glu	tta Leu 295	aag Lys	aaa Lys	aaa Lys	att Ile	aaa Lys 300	gag Glu	gct Ala	aag Lys	gat Asp	912

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Sub A1

tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt	960
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu	
305 310 315 320	
ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa	1008
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys	
325 330 335	
aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt	1056
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe	
340 345 350	
aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat	1104
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn	
355 360 365	
tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa	1152
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys	
370 375 380	
cct taa	1158
Pro *	
385	

<210> 56
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<400> 56

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Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala Leu	
35 40 45	
Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys Ile	
50 55 60	
His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser Leu	
65 70 75 80	
Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu Asp	
85 90 95	
Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys Lys	
100 105 110	
Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp Leu	
115 120 125	
Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu Lys	
130 135 140	
Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu Phe	
145 150 155 160	
Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala Asn	
165 170 175	
Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys	
180 185 190	
Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro	
195 200 205	
Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile	
210 215 220	

[illegible]

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Met	Cys	Ser	Asn	Ser	Gly	Lys	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro			
1				5					10					15				
gct	gac	gag	tct	gcg	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agc	aaa	aaa		96	
Ala	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys			
			20					25					30					
att	aca	gat	tct	aat	gca	ttt	gta	ctt	gct	gtt	aaa	gaa	ggt	gag	act		144	
Ile	Thr	Asp	Ser	Asn	Ala	Phe	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr			
		35					40					45						
ttg	gtt	tta	tct	ata	gat	gaa	ctt	gct	aag	aaa	gct	att	ggt	caa	aaa		192	
Leu	Val	Leu	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Lys	Ala	Ile	Gly	Gln	Lys			
	50					55					60							
ata	gac	aat	aat	aat	ggt	tta	gct	gct	tta	aat	aat	cag	aat	gga	tcg		240	
Ile	Asp	Asn	Asn	Asn	Gly	Leu	Ala	Ala	Leu	Asn	Asn	Gln	Asn	Gly	Ser			
65					70					75					80			
ttg	tta	gca	gga	gcc	tat	gca	ata	tca	acc	cta	ata	aca	gaa	aaa	ttg		288	
Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Thr	Glu	Lys	Leu			
				85					90					95				
agt	aaa	ttg	aaa	aat	tta	gaa	gaa	tta	aag	aca	gaa	att	gca	aag	gct		336	
Ser	Lys	Leu	Lys	Asn	Leu	Glu	Glu	Leu	Lys	Thr	Glu	Ile	Ala	Lys	Ala			
			100					105					110					

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca 384
 Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
 115 120 125
 gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att 432
 Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
 130 135 140
 tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat 480
 Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
 145 150 155 160
 tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta 528
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
 165 170 175
 act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca 576
 Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
 180 185 190
 aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act 624
 Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
 195 200 205
 aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa 672
 Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
 210 215 220
 aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag 720
 Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
 225 230 235 240
 gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 768
 Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
 245 250 255
 ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 816
 Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
 260 265 270
 ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 864
 Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Thr Gln Lys Leu
 275 280 285
 agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 912
 Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
 290 295 300
 gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 960
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
 305 310 315 320
 ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1008
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 325 330 335

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Sub A1

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<212> PRT
<213> ospC Chimera
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			20					25					30			
Ile	Thr	Asp	Ser	Asn	Ala	Phe	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	
		35					40					45				
Leu	Val	Leu	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Lys	Ala	Ile	Gly	Gln	Lys	
	50					55					60					
Ile	Asp	Asn	Asn	Asn	Gly	Leu	Ala	Ala	Leu	Asn	Asn	Gln	Asn	Gly	Ser	
65					70					75					80	
Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Thr	Glu	Lys	Leu	
				85					90					95		
Ser	Lys	Leu	Lys	Asn	Leu	Glu	Glu	Leu	Lys	Thr	Glu	Ile	Ala	Lys	Ala	
			100					105					110			
Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Gly	His	Ala	
		115					120					125				
Asp	Leu	Gly	Lys	Gln	Asp	Ala	Thr	Asp	Asp	His	Ala	Lys	Ala	Ala	Ile	
	130					135					140					
Leu	Lys	Thr	His	Ala	Thr	Thr	Asp	Lys	Gly	Ala	Lys	Glu	Phe	Lys	Asp	
145					150					155					160	
Leu	Phe	Glu	Ser	Val	Glu	Gly	Leu	Leu	Lys	Ala	Ala	Gln	Val	Ala	Leu	
				165					170					175		
Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	Val	Val	Ala	Glu	Ser	Pro	
			180					185					190			
Lys	Lys	Pro	His	Met	Ala	Asn	Asn	Ser	Gly	Gly	Asp	Ser	Ala	Ser	Thr	
		195					200					205				
Asn	Pro	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Val	Ile	Ser	Lys	
	210					215					220					
Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	Leu	Leu	Ala	Val	Lys	Glu	Val	Glu	
225					230					235					240	
Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Leu	Ser	Lys	Ala	Ile	Gly	Lys	Lys	
				245					250					255		
Ile	Lys	Asn	Asp	Gly	Thr	Leu	Asp	Asn	Glu	Ala	Asn	Arg	Asn	Glu	Ser	
			260					265					270			
Leu	Ile	Ala	Gly	Ala	Tyr	Glu	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	
		275					280					285				

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Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
 290 295 300
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
 305 310 315 320
 Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
 325 330 335
 Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
 340 345 350
 Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
 355 360 365
 Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
 370 375 380
 Lys Pro
 385

<210> 59
 <211> 1197
 <212> DNA
 <213> ospC Chimera

<220>
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 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

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SubA1

65/102

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205

cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat 672
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
 210 215 220

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 225 230 235 240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc 768
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 245 250 255

gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct 816
 Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala
 260 265 270

aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag 864
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu
 275 280 285

gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac 912
 Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn
 290 295 300

tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag 960
 Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys
 305 310 315 320

gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa 1008
 Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys
 325 330 335

tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
 340 345 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104
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 355 360 365

Sub-A1

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gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
 370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197
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 385 390 395

<210> 60
 <211> 398
 <212> PRT
 <213> ospC Chimera

<400> 60
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 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
 85 90 95
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
 100 105 110
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
 130 135 140
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
 145 150 155 160
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
 165 170 175
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
 180 185 190
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp Gly
 210 215 220
 Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
 225 230 235 240
 Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
 245 250 255
 Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys
 260 265 270
 Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala
 275 280 285
 Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu
 290 295 300
 Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala
 305 310 315 320
 Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu
 325 330 335

0055745-061900

SubA1

Sub-A1

Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn
 340 345 350
 Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala
 355 360 365
 Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala
 370 375 380
 Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

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 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160

006745-06100

Sub A1

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205

cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat 672
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
 210 215 220

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 225 230 235 240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg 768
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 245 250 255

gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct 816
 Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
 260 265 270

act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc 864
 Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val
 275 280 285

gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca 912
 Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 290 295 300

aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta 960
 Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu
 305 310 315 320

aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa 1008
 Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys
 325 330 335

aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat 1056
 Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp
 340 345 350

gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag 1104
 Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys
 355 360 365

ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca 1152
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala
 370 375 380

00596746-067900

Sub-A1

Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu	Ala	Lys
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Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu			
385					390					395					

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 <212> DNA
 <213> ospC Chimera

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1 5 10 15	
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
65 70 75 80	
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn	
85 90 95	
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100 105 110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115 120 125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130 135 140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag gcc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145 150 155 160	
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165 170 175	

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205

agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct 672
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
 210 215 220

gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
 225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa 768
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
 245 250 255

gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt 816
 Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly
 260 265 270

aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac 864
 Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn
 275 280 285

gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa 912
 Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys
 290 295 300

aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa 960
 Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu
 305 310 315 320

aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa 1008
 Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu
 325 330 335

cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa 1056
 His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys
 340 345 350

gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt 1104
 Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu
 355 360 365

gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gaa gct aaa gag 1152
 Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu
 370 375 380

atg ctt act aat tca gtt aaa gag ctt aca agc 1185
 Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

Sub-A1
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 <212> PRT
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 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
 85 90 95
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
 100 105 110
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
 130 135 140
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
 145 150 155 160
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
 165 170 175
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
 210 215 220
 Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
 225 230 235 240
 Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
 245 250 255
 Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
 260 265 270
 Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
 275 280 285
 Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
 290 295 300
 Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
 305 310 315 320
 Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
 325 330 335
 Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
 340 345 350
 Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
 355 360 365
 Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
 370 375 380
 Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390

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 <211> 1184

006790 9479550

<212> DNA
<213> ospC Chimera

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1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195 200 205

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SubA1

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[illegible]

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 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
 Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205

agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggc aat gca tct 672
 Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser
 210 215 220

00596746-051900

Sub A1

<400> 68															
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			20					25					30		
Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn
		35					40					45			
Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	Leu
	50					55					60				

78/102

Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
65 70 75 80
Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
85 90 95
Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
100 105 110
Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
115 120 125
Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
130 135 140
Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
145 150 155 160
Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
165 170 175
Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
180 185 190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195 200 205
Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr
210 215 220
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
225 230 235 240
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
245 250 255
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
260 265 270
Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr
275 280 285
Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys
290 295 300
Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala
305 310 315 320
Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala
325 330 335
Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile
340 345 350
Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys
355 360 365
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370 375 380
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385 390

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<220>
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1 5 10 15

Sub A1

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79/102													
ggt Gly 20	gct Ala	gag Glu	tca Ser	att Ile	gga Gly 25	tcc Ser	tgt Cys	aat Asn	aat Asn	tca Ser 30	ggg Gly	aaa Ala	aaa Ala
aca Thr	tct Ser	gca Ala	aat Asn	tct Ser 40	gct Ala	gat Asp	gag Glu	tct Ser	ggt Val 45	aaa Lys	ggg Gly	aaa Ala	aaa Ala
gaa Glu	ata Ile	agt Ser	aaa Lys 55	aaa Lys	att Ile	acg Thr	gat Asp	tct Ser 60	aat Asn	gcg Ala	ggt Val	aaa Ala	aaa Ala
aaa Lys	gag Glu	ggt Val 70	gaa Glu	gcg Ala	ttg Leu	ctg Leu	tca Ser 75	tct Ser	ata Ile	gat Asp	gag Glu	aaa Ala	aaa Ala
att Ile 85	ggt Gly	aaa Lys	aaa Lys	ata Ile	aaa Lys	aac Asn 90	gat Asp	ggt Gly	agt Ser	tta Leu	gat Asp 95	aaa Ala	aaa Ala
cgc Arg 100	aac Asn	gag Glu	tca Ser	ttg Leu	tta Leu 105	gca Ala	gga Gly	gct Ala	tat Tyr	aca Thr 110	ata Ile	aaa Ala	aaa Ala
aca Thr	caa Gln	aaa Lys	tta Leu	agt Ser 120	aaa Lys	tta Leu	aac Asn	gga Gly	tca Ser 125	gaa Glu	ggt Gly	aaa Ala	aaa Ala
att Ile	gcc Ala	gca Ala	gct Ala 135	aag Lys	aaa Lys	tgc Cys	tct Ser	gaa Glu 140	gag Glu	ttt Phe	agt Ser	aaa Ala	aaa Ala
gat Asp	aat Asn	cat His 150	gca Ala	cag Gln	ctt Leu	ggt Gly	ata Ile 155	cag Gln	ggc Gly	ggt Val	act Thr	aaa Ala	aaa Ala
aaa Lys 165	aaa Lys	gct Ala	att Ile	tta Leu	aaa Lys	gca Ala 170	aat Asn	gca Ala	gcg Ala	ggt Gly	aaa Lys 175	aaa Ala	aaa Ala
gaa Glu 180	gaa Glu	ctt Leu	gaa Glu	aag Lys	ttg Leu 185	tcc Ser	gga Gly	tca Ser	tta Leu	gaa Glu 190	agc Ser	aaa Ala	aaa Ala
gct Ala	aaa Lys	gag Glu	atg Met 200	ctt Leu	gct Ala	aat Asn	tca Ser	ggt Val 205	aaa Lys	gag Glu	ctt Leu	aaa Ala	aaa Ala
gtc Val	cat His	ggt Gly	aat Asn 215	aat Asn	tca Ser	ggt Gly	ggg Gly	gat Asp 220	tct Ser	gca Ala	tct Ser	aaa Ala	aaa Ala
gag Glu	tct Ser	gca Ala	aaa Lys 230	gga Gly	cct Pro	aat Asn	ctt Leu 235	acc Thr	gta Val	ata Ile	agc Ser	aaa Ala	aaa Ala
gat Asp 245	tct Ser	aat Asn	gca Ala	ttt Phe	tta Leu 250	ctg Leu	gct Ala	gtg Val	aaa Lys	gaa Glu	ggt Val 255	aaa Ala	aaa Ala

Sub A1

gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 816
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
260 265 270

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 864
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
275 280 285

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 912
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
290 295 300

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 960
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
305 310 315 320

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 1008
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
325 330 335

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1056
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
340 345 350

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1104
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
355 360 365

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1152
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
370 375 380

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1200
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
385 390 395 400

aaa cct taa 1209
Lys Pro *

<210> 70
<211> 401
<212> PRT
<213> ospC Chimera

<400> 70
Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
1 5 10 15
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
20 25 30
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
35 40 45
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
50 55 60
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala
65 70 75 80

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Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu
 85 90 95
 Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr
 100 105 110
 Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys
 130 135 140
 Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu
 145 150 155 160
 Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys
 165 170 175
 Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
 210 215 220
 Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
 225 230 235 240
 Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
 245 250 255
 Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile
 260 265 270
 Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 275 280 285
 Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
 290 295 300
 Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
 305 310 315 320
 Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
 325 330 335
 Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
 340 345 350
 Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
 355 360 365
 Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
 370 375 380
 Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
 385 390 395 400
 Pro

<210> 71
 <211> 1179
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1179)

<400> 71
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
 85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
 100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
 115 120 125

gaa aag att gat aca gct aag caa tct tct aca gaa ttt act aat aaa 432
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
 130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
 145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
 165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
 180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
 195 200 205

att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat 672
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
 210 215 220

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa 768
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
 245 250 255

006 000 000 000

Sub A1

act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa 816
 Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys
 260 265 270
 ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca 864
 Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser
 275 280 285
 tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata 912
 Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile
 290 295 300
 agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct 960
 Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala
 305 310 315 320
 aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca 1008
 Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr
 325 330 335
 gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att 1056
 Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile
 340 345 350
 tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag 1104
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys
 355 360 365
 tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt 1152
 Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu
 370 375 380
 act aat tca gtt aaa gag ctt aca agc 1179
 Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390

<210> 72
 <211> 392
 <212> PRT
 <213> ospC Chimera

<400> 72
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1 5 10 15
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 50 55 60
 Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn
 85 90 95
 Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp
 100 105 110

000130 94236560

Sub-A1

Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu
 115 120 125
 Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu
 130 135 140
 Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn
 145 150 155 160
 Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala
 165 170 175
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala
 180 185 190
 Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile
 195 200 205
 Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 210 215 220
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 225 230 235 240
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 245 250 255
 Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 260 265 270
 Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu
 275 280 285
 Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser
 290 295 300
 Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys
 305 310 315 320
 Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp
 325 330 335
 Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu
 340 345 350
 Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu
 355 360 365
 Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr
 370 375 380
 Asn Ser Val Lys Glu Leu Thr Ser
 385 390

<210> 73
 <211> 1178
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1178)

<400> 73
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat Asn	ctt Leu	aca Thr	gaa Glu	ata Ile	agt Ser	aaa Lys	aaa Lys	att Ile	aca Thr	gaa Glu	tct Ser	aac Asn	gca Ala	gtt Val	gtt Val	192
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ctg Leu	gcc Ala	gtg Val	aaa Lys	gaa Glu	gtt Val	gag Glu	acc Thr	tta Leu	ctt Leu	gca Ala	tct Ser	ata Ile	gat Asp	gaa Glu	ctt Leu	240
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gct Ala	acc Thr	aaa Lys	gct Ala	att Ile	ggg Gly	aaa Lys	aaa Lys	ata Ile	ggc Gly	aat Asn	aat Asn	ggg Gly	tta Leu	gag Glu	gcc Ala	288
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aat Asn	cag Gln	agt Ser	aaa Lys	aac Asn	aca Thr	tca Ser	ttg Leu	tta Leu	tca Ser	gga Gly	gct Ala	tat Tyr	gca Ala	ata Ile	tct Ser	336
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gac Asp	cta Leu	ata Ile	gca Ala	gaa Glu	aaa Lys	tta Leu	aat Asn	gta Val	ttg Leu	aaa Lys	aat Asn	gaa Glu	gaa Glu	tta Leu	aag Lys	384
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gaa Glu	aag Lys	att Ile	gat Asp	aca Thr	gct Ala	aag Lys	caa Gln	tgt Cys	tct Ser	aca Thr	gaa Glu	ttt Phe	act Thr	aat Asn	aaa Lys	432
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cta Leu	aaa Lys	agt Ser	gaa Glu	cat His	gca Ala	gtg Val	ctt Leu	ggg Gly	ctg Leu	gac Asp	aat Asn	ctt Leu	act Thr	gat Asp	gat Asp	480
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aat Asn	gca Ala	caa Gln	aga Arg	gct Ala	att Ile	tta Leu	aaa Lys	aaa Lys	cat His	gca Ala	aat Asn	aaa Lys	gat Asp	aag Lys	ggg Gly	528
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gct Ala	gca Ala	gaa Glu	ctt Leu	gaa Glu	aag Lys	tta Leu	ttt Phe	aaa Lys	gag Ala	gta Val	gaa Glu	aac Asn	tta Leu	tca Ser	aaa Lys	576
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gca Ala	gct Ala	caa Gln	gac Asp	aca Thr	tta Leu	aaa Lys	aat Asn	gct Ala	gtt Val	aaa Lys	gag Glu	ctt Leu	aca Thr	agt Ser	cct Pro	624
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att Ile	gtc Val	cat His	ggg Gly	aat Asn	aat Asn	tca Ser	gga Gly	aaa Lys	gat Asp	ggg Gly	aat Asn	aca Thr	tct Ser	gca Ala	aat Asn	672
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tct Ser	gct Ala	gat Asp	gag Glu	tct Ser	gtt Val	aaa Lys	ggg Gly	cct Pro	aat Asn	ctt Leu	aca Thr	gaa Glu	ata Ile	agt Ser	aaa Lys	720
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aaa Lys	att Ile	aca Thr	gaa Glu	tct Ser	aac Asn	gca Ala	gtt Val	gtt Val	ctg Leu	gct Ala	gtg Val	aaa Lys	gaa Glu	att Ile	gaa Glu	768
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act Thr	ttg Leu	ctt Leu	gca Ala	tct Ser	ata Ile	gat Asp	gaa Glu	ctt Leu	gct Ala	act Thr	aaa Lys	gct Ala	att Ile	ggg Gly	aaa Lys	816

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SubA1

aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga	864
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly	
275 280 285	
aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa	912
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys	
290 295 300	
tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn	
305 310 315 320	
gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His	
325 330 335	
gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala	
340 345 350	
att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355 360 365	
aag cta ttt aaa gca gta gaa aag ttg gca aaa gca gct aaa gag atg	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met	
370 375 380	
ctt gct aat tca gtt aaa gag ctt ac	1178
Leu Ala Asn Ser Val Lys Glu Leu	
385 390	

<210> 74
 <211> 391
 <212> PRT
 <213> ospC Chimera

<400> 74

Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala	
1 5 10 15	
Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp	
20 25 30	
Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
35 40 45	
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
50 55 60	
Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala	
65 70 75 80	
Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn	
85 90 95	
Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp	
100 105 110	
Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu	
115 120 125	
Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu	
130 135 140	
Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn	
145 150 155 160	

00595746-051900

Sub A1

Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala
165 170 175
Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala
180 185 190
Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile
195 200 205
Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
210 215 220
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
225 230 235 240
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr
245 250 255
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
260 265 270
Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr
275 280 285
Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu
290 295 300
Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala
305 310 315 320
Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala
325 330 335
Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile
340 345 350
Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys
355 360 365
Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu
370 375 380
Ala Asn Ser Val Lys Glu Leu
385 390

<210> 75
<211> 1178
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1178)

<400> 75
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
50 55 60

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ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu 65 70 75 80
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala 85 90 95
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser 100 105 110
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys 115 120 125
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys 130 135 140
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp 145 150 155 160
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly 165 170 175
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys 180 185 190
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro 195 200 205
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn 210 215 220
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys 225 230 235 240
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu 245 250 255
acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys 260 265 270
aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser 275 280 285
ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu 290 295 300

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag 960
 Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
 305 310 315 320
 caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg 1008
 Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
 325 330 335
 ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta 1056
 Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
 340 345 350
 aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta 1104
 Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
 355 360 365
 ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa 1152
 Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
 370 375 380
 aat gct gtt aaa gag ctt aca agt cc 1178
 Asn Ala Val Lys Glu Leu Thr Ser
 385 390

<210> 76
 <211> 391
 <212> PRT
 <213> ospC Chimera

<400> 76
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1 5 10 15
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 50 55 60
 Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
 65 70 75 80
 Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn
 85 90 95
 Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp
 100 105 110
 Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu
 115 120 125
 Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu
 130 135 140
 Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn
 145 150 155 160
 Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala
 165 170 175
 Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala
 180 185 190
 Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile
 195 200 205

005544061500

Sub A1

Sub-A1

Val	His	Gly	Asn	Asn	Ser	Arg	Lys	Asp	Gly	Asn	Ala	Ser	Thr	Asn	Ser
210						215				220					
Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys
225					230					235					240
Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr
				245					250					255	
Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys
			260					265					270		
Ile	Gly	Asn	Asn	Gly	Leu	Glu	Ala	Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu
	275						280					285			
Leu	Ser	Gly	Ala	Tyr	Ala	Ile	Ser	Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn
290						295					300				
Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln
305					310					315					320
Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Glu	His	Ala	Val	Leu
				325					330					335	
Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp	Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys
			340					345					350		
Lys	His	Ala	Asn	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe
	355						360					365			
Lys	Ala	Val	Glu	Asn	Leu	Ser	Lys	Ala	Ala	Gln	Asp	Thr	Leu	Lys	Asn
370						375					380				
Ala	Val	Lys	Glu	Leu	Thr	Ser									
385					390										

<210> 77
 <211> 1230
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 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1230)

<400> 77
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160

gct gat gca aaa gaa ggc att tta aaa aca aat ggt act aaa act aaa 528
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205

cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca 672
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser
 210 215 220

ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct 720
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro
 225 230 235 240

aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta 768
 Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu
 245 250 255

ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt 816
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 260 265 270

tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac 864
 Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn
 275 280 285

gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca 912
 Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser
 290 295 300

aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag 960
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys
 305 310 315 320

00596746-051900

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Sub A1

aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag 1008
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys
 325 330 335

cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat 1056
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp
 340 345 350

aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt 1104
 Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly
 355 360 365

gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa 1152
 Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys
 370 375 380

gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct 1200
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro
 385 390 395 400

gtt gtg gca gaa agt cca aaa aaa cct taa 1230
 Val Val Ala Glu Ser Pro Lys Lys Pro *

<210> 78
 <211> 408
 <212> PRT
 <213> ospC Chimera

<400> 78
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
 1 5 10 15
 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
 85 90 95
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
 100 105 110
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
 130 135 140
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
 145 150 155 160
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
 165 170 175
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
 180 185 190
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser Gly
 210 215 220

006799-06100

Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn
 225 230 235 240
 Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu
 245 250 255
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser
 260 265 270
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu
 275 280 285
 Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys
 290 295 300
 Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys
 305 310 315 320
 Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu
 325 330 335
 Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn
 340 345 350
 Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala
 355 360 365
 Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala
 370 375 380
 Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val
 385 390 395 400
 Val Ala Glu Ser Pro Lys Lys Pro
 405

<210> 79
 <211> 1209
 <212> DNA
 <213> ospC Chimera

<220>
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 <222> (1)...(1209)

<400> 79
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
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 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205

cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
 210 215 220

ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 225 230 235 240

ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca 768
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 245 250 255

gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat 816
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
 260 265 270

gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta 864
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
 275 280 285

gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta 912
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
 290 295 300

att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga 960
 Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
 305 310 315 320

gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt 1008

0067450500

Sub A1

Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
 325 330 335
 act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt 1056
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
 340 345 350
 act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa 1104
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
 355 360 365
 act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac 1152
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
 370 375 380
 ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt 1200
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
 385 390 395 400
 aca agc taa 1209
 Thr Ser *

<210> 80
 <211> 401
 <212> PRT
 <213> ospC Chimera

<400> 80
 Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala
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 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys Asp
 20 25 30
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 35 40 45
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu
 50 55 60
 Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr
 85 90 95
 Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser
 100 105 110
 Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys
 115 120 125
 Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys
 130 135 140
 Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala
 145 150 155 160
 Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly
 165 170 175
 Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys
 180 185 190
 Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly
 210 215 220

Sub A1

00596746-054000

SubA1

Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
 225 230 235 240
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
 245 250 255
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu
 260 265 270
 Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp
 275 280 285
 Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile
 290 295 300
 Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu
 305 310 315 320
 Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
 325 330 335
 Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr
 340 345 350
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr
 355 360 365
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
 370 375 380
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
 385 390 395 400
 Ser

<210> 81
 <211> 1205
 <212> DNA
 <213> ospC Chimera

<220>
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc	gaa	tat	aat	cac	aat	gga	tca	ttg	tta	gcg	gga	gct	tat	gca	ata	336
Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	
			100							105				110		
tca	acc	cta	ata	aaa	caa	aaa	tta	gat	gga	ttg	aaa	aat	gaa	gga	tta	384
Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	
			115							120				125		
aag	gaa	aaa	att	gat	gcg	gct	aag	aaa	tgt	tct	gaa	aca	ttt	act	aat	432
Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn	
			130							135				140		
aaa	tta	aaa	gaa	aaa	cac	aca	gat	ctt	ggt	aaa	gaa	ggt	gtt	act	gat	480
Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	
			145							150				155		
gct	gat	gca	aaa	gaa	gcc	att	tta	aaa	aca	aat	ggt	act	aaa	act	aaa	528
Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys	Thr	Asn	Gly	Thr	Lys	Thr	Lys	
			165							170				175		
ggt	gct	gaa	gaa	ctt	gga	aaa	tta	ttt	gaa	tca	gta	gag	gtc	ttg	tca	576
Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	
			180							185				190		
aaa	gca	gct	aaa	gag	atg	ctt	gct	aat	tca	gtt	aaa	gag	ctt	aca	agc	624
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	
			195							200				205		
cct	gtt	gtg	gca	gaa	agt	cca	aaa	aaa	cct	tcc	atg	gta	aat	aat	tca	672
Pro	Val	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	Ser	Met	Val	Asn	Asn	Ser	
			210							215				220		
gga	aaa	gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	720
Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	
			225							230				235		
ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	gca	768
Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	
			245							250				255		
gtt	gtt	ctg	gct	gtg	aaa	gaa	att	gaa	act	ttg	ctt	gca	tct	ata	gat	816
Val	Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	
			260							265				270		
gaa	ctt	gct	act	aaa	gct	att	ggt	aaa	aaa	ata	caa	caa	aat	ggt	ggt	864
Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn	Gly	Gly	
			275							280				285		
tta	gct	gtc	gaa	gcg	ggg	cat	aat	gga	aca	ttg	tta	gca	ggt	gct	tat	912
Leu	Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly	Ala	Tyr	
			290							295				300		
aca	ata	tca	aaa	cta	ata	aca	caa	aaa	tta	gat	gga	ttg	aaa	aat	tca	960
Thr	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Ser	
			305							310				315		

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Sub A1

gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat	1008
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp	
325 330 335	
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat	1056
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn	
340 345 350	
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct	1104
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala	
355 360 365	
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa	1152
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu	
370 375 380	
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag	1200
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu	
385 390 395 400	
ctt ac	1205
Leu	

<210> 82
 <211> 400
 <212> PRT
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<400> 82

Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys Ala	
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20 25 30	
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
35 40 45	
Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu	
50 55 60	
Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile Ala	
65 70 75 80	
Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr	
85 90 95	
Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser	
100 105 110	
Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys	
115 120 125	
Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys	
130 135 140	
Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala	
145 150 155 160	
Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly	
165 170 175	
Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys	
180 185 190	
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro	
195 200 205	
Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser Gly	
210 215 220	

006T99-05100

2025年12月25日
 星期四
 晴
 12月25日
 星期四
 晴
 12月25日
 星期四
 晴

<400>	83																
atg	aga	tta	tta	ata	gga	ttt	gct	tta	gcg	tta	gct	tta	ata	gga	tgt		48
Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys		
1				5					10					15			
gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	agt	aat	tca	ggg	aaa		96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Ser	Asn	Ser	Gly	Lys		
			20					25					30				
ggt	ggg	gat	tct	gca	tct	act	aat	cct	gct	gac	gag	tct	gcg	aaa	ggg		144
Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	Ala	Asp	Glu	Ser	Ala	Lys	Gly		
		35					40					45					
cct	aat	ctt	aca	gaa	ata	agc	aaa	aaa	att	aca	gat	tct	aat	gca	ttt		192
Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe		
	50					55					60						
gta	ctt	gct	gtt	aaa	gaa	gtt	gag	act	ttg	gtt	tta	tct	ata	gat	gaa		240
Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Val	Leu	Ser	Ile	Asp	Glu		
65				70						75					80		
ctt	gct	aag	aaa	gct	att	ggt	caa	aaa	ata	gac	aat	aat	aat	ggt	tta		288
Leu	Ala	Lys	Lys	Ala	Ile	Gly	Gln	Lys	Ile	Asp	Asn	Asn	Asn	Gly	Leu		
				85					90					95			

100/102

gct gct tta aat aat cag aat gga tcg ttg tta gca gga gcc tat gca 336
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala
100 105 110

ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa 384
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu
115 120 125

gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt 432
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe
130 135 140

act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct 480
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala
145 150 155 160

acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc 528
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr
165 170 175

gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt 576
Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly
180 185 190

ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt 624
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu
195 200 205

aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat 672
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn
210 215 220

aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa 720
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys
225 230 235 240

gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca 768
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala
245 250 255

ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat 816
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp
260 265 270

gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta 864
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu
275 280 285

gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa 912
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu
290 295 300

ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa 960
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu
305 310 315 320

tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act 1008
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr
325 330 335

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Sub A1

act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag 1056
 Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln
 340 345 350
 gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac 1104
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp
 355 360 365
 aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg 1152
 Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu
 370 375 380
 tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca 1200
 Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
 385 390 395 400
 aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 1236
 Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
 405 410

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 <211> 410
 <212> PRT
 <213> ospC Chimera

<400> 84
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 Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys Gly
 20 25 30
 Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Val
 50 55 60
 Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Gly Leu Ala
 85 90 95
 Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu Glu
 115 120 125
 Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
 130 135 140
 Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala Thr
 145 150 155 160
 Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr Asp
 165 170 175
 Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly Leu
 180 185 190
 Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
 195 200 205
 Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn Asn
 210 215 220
 Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
 225 230 235 240

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Sub A1

Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 245 250 255
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
 260 265 270
 Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
 275 280 285
 Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
 290 295 300
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
 305 310 315 320
 Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
 325 330 335
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
 340 345 350
 Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
 355 360 365
 Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
 370 375 380
 Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
 385 390 395 400
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 405 410

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Sub A1